

(a) a region of the nucleotide sequence of SEQ ID NO: 1 encoding a polypeptide fragment of at least 25 amino acid residues;

(b) a region of the nucleotide sequence of SEQ ID NO: 1 comprising a fragment of at least 16 nucleotides;

(c) a nucleotide sequence that hybridizes under at least moderately stringent conditions to the complement of the nucleotide sequence of either (a) or (b); or

(d) a nucleotide sequence complementary to the nucleotide sequence of any of (a) - (c).

3. (Amended) An isolated nucleic acid molecule comprising:

(a) a nucleotide sequence encoding a polypeptide as set forth in SEQ ID NO: 2 with at least one conservative amino acid substitution, wherein the encoded polypeptide is at least 70 percent identical to the polypeptide set forth in SEQ ID NO: 2;

(b) a nucleotide sequence encoding a polypeptide as set forth in SEQ ID NO: 2 having a C- and/or N- terminal truncation, wherein the encoded polypeptide comprises at least 25 amino acid residues;

(c) a nucleotide sequence encoding a polypeptide as set forth in SEQ ID NO: 2 with at least one modification that is a conservative amino acid substitution, C-terminal truncation, or N-terminal truncation, wherein the encoded polypeptide is at least 70 percent identical to the polypeptide set forth in SEQ ID NO: 2 and comprises at least 25 amino acid residues;

(d) a region of the nucleotide sequence of any of (a) - (c) comprising a fragment of at least 16 nucleotides;

(e) a nucleotide sequence that hybridizes under at least moderately stringent conditions to the complement of the nucleotide sequence of any of (a) - (d); or

(f) a nucleotide sequence complementary to the nucleotide sequence of any of (a) - (e).

10. (Amended) The process of Claim 8, wherein the nucleic acid molecule

DOES NOT COMPREHEND THE SEQUENCE OF THE NUCLEOTIDE SEQUENCE OF SEQ ID NO: 1.

11. (Amended) The isolated nucleic acid molecule according to Claim 2, wherein the percent identity is determined using a computer program that is GAP, BLASTN, FASTA, BLASTA, BLASTX, BestFit, or the Smith-Waterman algorithm.

45. (Amended) A nucleic acid molecule encoding a fusion polypeptide comprising the nucleic acid molecule of any of Claims 1, 2, or 3 fused to DNA encoding a heterologous amino acid sequence.

46. (Amended) The nucleic acid molecule of Claim 45, wherein the DNA encoding the heterologous amino acid sequence encodes an IgG constant domain or biologically active fragment thereof.

Please cancel claims 9, 12-41, and 47-54 without prejudice or disclaimer.

REMARKS

Claims 1-3, 10, 11, 45, and 46, as amended, and claims 4-8 and 42-44, as filed, are pending in this application. Claims 9, 12-41, and 47-54 have been canceled without prejudice or disclaimer. No new matter has been added as a result of the above-described amendments. Support for the amendments to the claims can be found in the specification at, for example, page 18, lines 23-27. The rejections set forth in the Office Action have been overcome by amendment or are traversed by argument below.

1. Substitution of New Title

The Office Action states that a new title is required that is clearly indicative of the invention to which the claims are directed. Applicants have amended the title to read: "Nucleic Acids Encoding Interleukin-1 Receptor Antagonist-Like Proteins and Uses Thereof," which Applicants contend is clearly indicative of the invention to which the claims are directed.